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  - Bruker XWinNMR and UXNMR
- UCSF NMR format
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- Sparky project files

Output

- Peak lists
- Chemical shift list
- Chemical shift table

File commands

file open...	fo	open UCSF NMR data, a Felix matrix, or a Sparky spectrum file
file save	fs	save a Sparky spectrum annotation file
file save as...	fa	save spectrum with a new name
project open...	jo	open several spectra at once
project save	js	save all spectra
project save as...	ja	save project with a new name
preferences...	pf	miscellaneous settings
quit	qt	

View commands

axes in Hertz	xh	display view scale axes in Hz
axes in ppm	xp	display view scale axes in parts per million
axes show index	xd	show data index values on view scales
axis nucleus types	xa	show nucleus type (1H, 13C, 15N) on axes
axis roll	xr	exchange axes keeping center point of fixed
axis transpose	xx	zoom to cross-diagonal region of spectrum
center view on peak	vc	center a view on the selected peak
orthogonal views	ov	show 3 orthogonal views of a 3-D spectrum
region goto	rg	zoom to a named region
region tool...	rt	name regions of a spectrum

renumber view	rv	renumber view name to use lowest available suffix number
show axis scales	vs	show scales (ppm, hz, or index units) along view axes
show grids	gs	toggle display of grids
show labels	ls	toggle display of labels
show lines	is	toggle display of lines
show ornaments	os	toggle display of all ornaments
show peaks	ps	toggle display of peaks
show peak groups	xs	toggle display of peak groups
show peak info	vp	show peak position / height / linewidth in status bar
show resonances	vR	show resonances along edge of spectrum
show scrollbars	vb	show scrollbars for view windows
show slices	vS	show 1-D data cross-sections along edge of spectrum
view duplicate	vd	make another view window
view hide	vh	undisplay a view
view redraw	vr	redraw the view (in case it gets messed up)
view settings...	vt	set crosshairs, aspect ratio, slices, ...
zoom full	zf	show entire spectrum
zoom in	zi	zoom in by a factor of 2
zoom out	zo	zoom out by a factor of 2
zoom down	zd	move down a plane in a 3D spectra
zoom up	zu	move up a plane in a 3D spectra
zoom previous	zp	zoom to the previously shown region
zoom next	zn	reverse of zoom previous (zp) command

Peak commands

add sweepwidth	a1 a2 a3 a4	adjust peak w1,w2,w3,w4 frequency one sweepwidth downfield
subtract sweepwidth	A1 A2 A3 A4	adjust peak w1,w2,w3,w4 frequency one sweepwidth upfield
reflect upfield	u1 u2 u3 u4	reflect peak w1,w2,w3,w4 frequency about upfield boundary
reflect upfield	d1 d2 d3 d4	reflect peak w1,w2,w3,w4 frequency about downfield boundary
assignment copy	ac	remember peak assignments for assignment paste
assignment delete	aD	delete the assignments of selected peaks
assignment paste	aP	paste assignments onto peaks in this spectrum
assignment paste & label	ap	copy assignments and show labels
crossdiagonal assignment copy	aX	copy assignments from crossdiagonal peaks
assignment tool...	at	make assignments
delete unused resonances	dr	delete resonances not used in any peak assignments
integration tool...	it	select integration method
sum over box method	ib	switch to box integration method

sum over ellipse method	ie	switch to ellipse integration method
Gaussian fit method	ig	switch to Gaussian fit integration
Lorentzian fit method	il	switch to Lorentzian fit integration
integrate selected peaks	pi	
ornament copy	oc	record ornaments for future paste operation
ornament paste	op	paste ornaments into this spectrum
crossdiagonal ornament copy	oX	copy ornaments across diagonal of 2D homonuclear spectrum
center peaks	pc	center selected peaks at local maxima or minima.
estimate linewidths	pe	get linewidth of selected peaks as width at half max
group peaks	pg	create a peak group from selected peaks
update heights	ph	reread peak heights from NMR data file
label peak	pl	put a label on a peak using a dialog
label peaks	lb	put assignment labels on selected peaks
unlabel peaks	lB	Remove labels from selected peaks
unoverlap labels	lu	move labels so they don't overlap each other
right offset labels	lr	move labels so they are to the right of peak markers
lock peaks	pk	prevent peaks from moving when integrated
select all peaks	pa	select all peaks in a spectrum
select fully assigned	pF	select fully assigned peaks
select partially assigned	pP	select partially assigned peaks
select unassigned	pN	select unassigned peaks
select by color	pC	select peaks by color
invert peak selection	pI	invert peak selection
select aliased	pA	select aliased peaks
select intra-residue	pR	select i to i assigned peaks
select sequential	pS	select i to i+1 assigned peaks
select medium range	pM	select i to i+2, i+3 or i+4 assigned peaks
select long range	pL	select i to i+5, i+6, ... assigned peaks
unintegrate peaks	pU	forget that a peak has been integrated
unlock peaks	pu	allow selected peaks to move when integrated
undo	eu	undo last peak move, deletion, or integration
w1 resonance peaks	r1	list assigned peaks with selected peak w1 resonance
w2 resonance peaks	r2	show assigments with selected peak w2 resonance
w3 resonance peaks	r3	show assigments with selected peak w3 resonance

Dialogs

assignment...	at	make assignments
assignment copy...	co	thresholds for copying assignments
assignment table...	tb	table of chemical shifts
contour levels...	ct	set contour levels and colors

integration...	it	set integration method
midas...	mi	display assignments on a structure using Midas
ornament...	ot	change ornament colors and sizes
note...	nt	add notes to peaks
overlay views...	ol	overlay contours of one spectrum on another
peak list...	lt	show a list of peaks for a spectrum
peak picking...	kt	set thresholds for find peak pointer mode
pointer modes...	pm	show buttons to select pointer mode
predefined resonances...	pd	copy resonances from another spectrum
preferences...	pf	set global Sparky options
print view...	pt	print spectrum views to a Postscript printer
project view list...	pv	list of views, sizes, peak counts, ...
python...	py	Python shell for running your own programs
region...	rt	name regions and apply operations to regions
rename resonances...	rr	rename atoms and groups
resonance list...	rl	list group/atom chemical shifts, standard deviations
spectrum...	st	set molecule and condition, and axis shifts
synchronize views...	yt	make views scroll in parallel
view...	vt	options controlling what is displayed in a view

Pointer Modes

select	F1	click or drag to select or move peaks, labels, lines, ...
center	F2	clicking centers view on point
add grid both	F3	place vertical and horizontal grid lines
add grid horz	F4	add a line extending across whole spectrum
add grid vert	F5	add a line extending across whole spectrum
add label	F6	add a text label to a peak
add line	F7	add a horizontal or vertical line between end points
find / add peak	F8	click to place a peak or drag to find peaks
integrate	F10	click or drag to integrate peaks
zoom	F11	drag to select a new region to show
duplicate and zoom	F12	drag to zoom and duplicate a view
assignment copy	sh-F1	copy assignments from an already assigned spectrum
assignment guess	sh-F2	make assignment if there is a unique guess